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Genetic strategy for identification of genes involved in citrus salt stress tolerance: status of genome mapping program

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ABSTRACT: Salt stress is one of the most obvious effects of high salinity on *Citrus*, which is classified among the most sensitive tree crops. Genetic and genomic analysis of tolerant and sensitive plants is a prerequisite for breeding programs and the selection of more adapted varieties to high salinity. The combined approach of genetic mapping and localization of candidate genes has been applied in plant genetics in the past decade with the objective of characterizing and cloning quantitative trait loci (QTLs). The segregation of the tolerance/ sensitivity to salt character was initiated on the F2 population resulting from the crossing Cleopatra mandarin X *Poncirus trifoliata*. Citrus linkage map was derived from the segregation analysis of SSR markers from EST or BAC ends. From many polymorphic primers only few makers have Mendelian segregation. The skewed segregation can be due to abnormal meiosis at the intergeneric level. The excess of homozygous locus was observed only for the marker CiBE2626b. No difference was observed between frequency of alleles from Poncirus and alleles from mandarin in homozygous loci. Half of F2 population (61 hybrids) has a percentage of homozygous loci lower than or equal to 20%. Other hybrids seem to have proportions of homozygous and heterozygous loci that follow a normal distribution although there is a slight shift of some homozygote individuals to represent the expected Gaussian curve (~ 0.45 instead of 0.5). We have also studied the segregation and mapped several candidate genes putatively involved in salinity tolerance. We plan to confirm the role played by these genes by gene expression analysis from selected homozygous F2 genotypes under strong salt stress conditions. We will measure the effects of salt stress on physiological traits on the segregating population.